Poster II-58

Evaluation of Extensible Markup Languages for High-Level Integrative Physiological Models*
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Sharing of data using common language standards is an important component of scientific data integration. In support of various large scale integrated modeling efforts including the Digital Human, supported by the Federation of American Scientists, and DARPA's Virtual Soldier, Oak Ridge National Laboratory is in the process of evaluating the present use of Extensible Markup Languages (XMLs) for high-level integrative physiological (HIP) models. This evaluation will support: 1) further development of and use of various XMLs within those projects; and 2) help with translating ontologies of anatomy and physiology, associated with these projects, into XML that can be utilized by the HIP models. This effort will be outlined at the BISTI Symposium and specific examples of XMLs (cellML, SBML, and physioML) will be compared. Cell Markup Language (CellML) is an XML for biological modeling (http://www.cellml.org/) and Systems Biology Markup Language (SBML) is an XML-based description language for representing computational models in systems biology (http://sourceforge.net/projects/sbml). Physiological Markup Language (physioML)[1] is an XML-based description language for representing physiological, pharmacokinetic, and kinetic modeling. The eventual integration of these various efforts into a common modeling XML for HIP models will be addressed. The ability to conduct integrative human modeling across a wide range of spatial and temporal scales will depend on establishing a common means of data sharing (i.e. adopting a common XML language).

Reference

R. C. Ward and N. B. Munro, "PhysioML - An Extensible Markup Language for Physiological Modeling," a presentation at the *Biomedical Engineering Society Annual Fall Meeting*, Nashville, TN, October 3, 2003 (Poster 7.P2.10). See also (http://www.ornl.gov/virtualhuman/physioml/).